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(1) GENERAL INFORMATION:

- (i) APPLICANT: WILLIAMS, Lewis T.
ESCOBEDO, Jaime A.
- (ii) TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Townsend and Townsend and Crew
 - (B) STREET: One Market, Steuart Street Tower, 20th Floor
 - (C) CITY: San Francisco
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94105
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/461,917
 - (B) FILING DATE: 05-JUN-1995
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/309,322
 - (B) FILING DATE: 10-FEB-1989
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/151,414
 - (B) FILING DATE: 02-FEB-1988
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Dow, Karen B.
 - (B) REGISTRATION NUMBER: 29,684
 - (C) REFERENCE/DOCKET NUMBER: 2307K-267-2-4
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415/326-2400
 - (B) TELEFAX: 415/326-2422

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6373 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 129..3398
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTGGAGCTAC AGGGAGAGAA ACAGAGGAGG AGACTGCAAG AGATCATTGG AGGCCGTGGG	60
CACGCTCTTT ACTCCATGTG TGGGACATTC ATTGCGGAAT AACATCGGAG GAGAAGTTTC	120
CCAGAGCT ATG GGG ACT TCC CAT CCG GCG TTC CTG GTC TTA GGC TGT CTT Met Gly Thr Ser His Pro Ala Phe Leu Val Leu Gly Cys Leu 1 5 10	170
CTC ACA GGG CTG AGC CTA ATC CTC TGC CAG CTT TCA TTA CCC TCT ATC Leu Thr Gly Leu Ser Leu Ile Leu Cys Gln Leu Ser Leu Pro Ser Ile 15 20 25 30	218
CTT CCA AAT GAA AAT GAA AAG GTT GTG CAG CTG AAT TCA TCC TTT TCT Leu Pro Asn Glu Asn Glu Lys Val Val Gln Leu Asn Ser Ser Phe Ser 35 40 45	266
CTG AGA TGC TTT GGG GAG AGT GAA GTG AGC TGG CAG TAC CCC ATG TCT Leu Arg Cys Phe Gly Glu Ser Glu Val Ser Trp Gln Tyr Pro Met Ser 50 55 60	314
GAA GAA GAG AGC TCC GAT GTG GAA ATC AGA AAT GAA GAA AAC AAC AGC Glu Glu Glu Ser Ser Asp Val Glu Ile Arg Asn Glu Glu Asn Asn Ser 65 70 75	362
GGC CTT TTT GTG ACG GTC TTG GAA GTG AGC AGT GCC TCG GCG GCC CAC Gly Leu Phe Val Thr Val Leu Glu Val Ser Ser Ala Ser Ala Ala His 80 85 90	410
ACA GGG TTG TAC ACT TGC TAT TAC AAC CAC ACT CAG ACA GAA GAG AAT Thr Gly Leu Tyr Thr Cys Tyr Tyr Asn His Thr Gln Thr Glu Glu Asn 95 100 105 110	458
GAG CTT GAA GGC AGG CAC ATT TAC ATC TAT GTG CCA GAC CCA GAT GTA Glu Leu Glu Gly Arg His Ile Tyr Ile Tyr Val Pro Asp Pro Asp Val 115 120 125	506
GCC TTT GTA CCT CTA GGA ATG ACG GAT TAT TTA GTC ATC GTG GAG GAT Ala Phe Val Pro Leu Gly Met Thr Asp Tyr Leu Val Ile Val Glu Asp 130 135 140	554
GAT GAT TCT GCC ATT ATA CCT TGT CGC ACA ACT GAT CCC GAG ACT CCT Asp Asp Ser Ala Ile Ile Pro Cys Arg Thr Thr Asp Pro Glu Thr Pro 145 150 155	602
GTA ACC TTA CAC AAC AGT GAG GGG GTG GTA CCT GCC TCC TAC GAC AGC Val Thr Leu His Asn Ser Glu Gly Val Val Pro Ala Ser Tyr Asp Ser 160 165 170	650
AGA CAG GGC TTT AAT GGG ACC TTC ACT GTA GGG CCC TAT ATC TGT GAG Arg Gln Gly Phe Asn Gly Thr Phe Thr Val Gly Pro Tyr Ile Cys Glu 175 180 185 190	698
GCC ACC GTC AAA GGA AAG AAG TTC CAG ACC ATC CCA TTT AAT GTT TAT Ala Thr Val Lys Gly Lys Lys Phe Gln Thr Ile Pro Phe Asn Val Tyr 195 200 205	746
GCT TTA AAA GCA ACA TCA GAG CTG GAT CTA GAA ATG GAA GCT CTT AAA Ala Leu Lys Ala Thr Ser Glu Leu Asp Leu Glu Met Glu Ala Leu Lys 210 215 220	794
ACC GTG TAT AAG TCA GGG GAA ACG ATT GTG GTC ACC TGT GCT GTT TTT Thr Val Tyr Lys Ser Gly Glu Thr Ile Val Val Thr Cys Ala Val Phe 225 230 235	842
AAC AAT GAG GTG GTT GAC CTT CAA TGG ACT TAC CCT GGA GAA GTG AAA Asn Asn Glu Val Val Asp Leu Gln Trp Thr Tyr Pro Gly Glu Val Lys 240 245 250	890

GGC Gly 255	AAA Lys	GGC Gly	ATC Ile	ACA Thr	ATG Met	CTG Leu	GAA Glu	GAA Glu	ATC Ile	AAA Lys	GTC Val	CCA Pro	TCC Ser	ATC Ile	AAA Lys	938
TTG Leu	GTG Val	TAC Tyr	ACT Thr	TTG Leu	ACG Thr	GTC Val	CCC Pro	GAG Glu	GCC Ala	ACG Thr	GTG Val	AAA Lys	GAC Asp	AGT Ser	GGA Gly	986
GAT Asp	TAC Tyr	GAA Glu	TGT Cys	GCT Ala	GCC Ala	CGC Arg	CAG Gln	GCT Ala	ACC Thr	AGG Arg	GAG Glu	GTC Val	AAA Lys	GAA Glu	ATG Met	1034
AAG Lys	AAA Lys	GTC Val	ACT Thr	ATT Ile	TCT Ser	GTC Val	CAT His	GAG Glu	AAA Lys	GGT Gly	TTC Phe	ATT Ile	GAA Glu	ATC Ile	AAA Lys	1082
CCC Pro	ACC Thr	TTC Phe	AGC Ser	CAG Gln	TTG Leu	GAA Glu	GCT Ala	GTC Val	AAC Asn	CTG Leu	CAT His	GAA Glu	GTC Val	AAA Lys	CAT His	1130
TTT Phe	GTT Val	GTA Val	GAG Glu	GTG Val	CGG Arg	GCC Ala	TAC Tyr	CCA Pro	CCT Pro	CCC Pro	AGG Arg	ATA Ile	TCC Ser	TGG Trp	CTG Leu	1178
AAA Lys	AAC Asn	AAT Asn	CTG Leu	ACT Thr	CTG Leu	ATT Ile	GAA Glu	AAT Asn	CTC Leu	ACT Thr	GAG Glu	ATC Ile	ACC Thr	ACT Thr	GAT Asp	1226
GTG Val	GAA Glu	AAG Lys	ATT Ile	CAG Gln	GAA Glu	ATA Ile	AGG Arg	TAT Tyr	CGA Arg	AGC Ser	AAA Lys	TTA Leu	AAG Lys	CTG Leu	ATC Ile	1274
CGT Arg	GCT Ala	AAG Lys	GAA Glu	GAA Glu	GAC Asp	AGT Ser	GGC Gly	CAT His	TAT Tyr	ACT Thr	ATT Ile	GTA Val	GCT Ala	CAA Gln	AAT Asn	1322
GAA Glu	GAT Asp	GCT Ala	GTG Val	AAG Lys	AGC Ser	TAT Tyr	ACT Thr	TTT Phe	GAA Glu	CTG Leu	TTA Leu	ACT Thr	CAA Gln	GTT Val	CCT Pro	1370
TCA Ser	TCC Ser	ATT Ile	CTG Leu	GAC Asp	TTG Leu	GTC Val	GAT Asp	GAT Asp	CAC His	CAT His	GGC Gly	TCA Ser	ACT Thr	GGG Gly	GGA Gly	1418
CAG Gln	ACG Thr	GTG Val	AGG Arg	TGC Cys	ACA Thr	GCT Ala	GAA Glu	GGC Gly	ACG Thr	CCG Pro	CTT Leu	CCT Pro	GAT Asp	ATT Ile	GAG Glu	1466
TGG Trp	ATG Met	ATA Ile	TGC Cys	AAA Lys	GAT Asp	ATT Ile	AAG Lys	AAA Lys	TGT Cys	AAT Asn	AAT Asn	GAA Glu	ACT Thr	TCC Ser	TGG Trp	1514
ACT Thr	ATT Ile	TTG Leu	GCC Ala	AAC Asn	AAT Asn	GTC Val	TCA Ser	AAC Asn	ATC Ile	ATC Ile	ACG Thr	GAG Glu	ATC Ile	CAC His	TCC Ser	1562
CGA Arg	GAC Asp	AGG Arg	AGT Ser	ACC Thr	GTG Val	GAG Glu	GGC Gly	CGT Arg	GTG Val	ACT Thr	TTC Phe	GCC Ala	AAA Lys	GTG Val	GAG Glu	1610
GAG Glu	ACC Thr	ATC Ile	GCC Ala	GTG Val	CGA Arg	TGC Cys	CTG Leu	GCT Ala	AAG Lys	AAT Asn	CTC Leu	CTT Leu	GGA Gly	GCT Ala	GAG Glu	1658
AAC Asn	CGA Arg	GAG Glu	CTG Leu	AAG Lys	CTG Leu	GTG Val	GCT Ala	CCC Pro	ACC Thr	CTG Leu	CGT Arg	TCT Ser	GAA Glu	CTC Leu	ACG Thr	1706

GTG	GCT	GCT	GCA	GTC	CTG	GTG	CTG	TTG	GTG	ATT	GTG	ATC	ATC	TCA	CTT	1754
Val	Ala	Ala	Ala	Val	Leu	Val	Leu	Leu	Val	Ile	Val	Ile	Ile	Ser	Leu	
			530					535					540			
ATT	GTC	CTG	GTT	GTC	ATT	TGG	AAA	CAG	AAA	CCG	AGG	TAT	GAA	ATT	CGC	1802
Ile	Val	Leu	Val	Val	Ile	Trp	Lys	Gln	Lys	Pro	Arg	Tyr	Glu	Ile	Arg	
		545					550					555				
TGG	AGG	GTC	ATT	GAA	TCA	ATC	AGC	CCA	GAT	GGA	CAT	GAA	TAT	ATT	TAT	1850
Trp	Arg	Val	Ile	Glu	Ser	Ile	Ser	Pro	Asp	Gly	His	Glu	Tyr	Ile	Tyr	
	560					565					570					
GTG	GAC	CCG	ATG	CAG	CTG	CCT	TAT	GAC	TCA	AGA	TGG	GAG	TTT	CCA	AGA	1898
Val	Asp	Pro	Met	Gln	Leu	Pro	Tyr	Asp	Ser	Arg	Trp	Glu	Phe	Pro	Arg	
575				580						585					590	
GAT	GGA	CTA	GTG	CTT	GGT	CGG	GTC	TTG	GGG	TCT	GGA	GCG	TTT	GGG	AAG	1946
Asp	Gly	Leu	Val	Leu	Gly	Arg	Val	Leu	Gly	Ser	Gly	Ala	Phe	Gly	Lys	
				595					600					605		
GTG	GTT	GAA	GGA	ACA	GCC	TAT	GGA	TTA	AGC	CGG	TCC	CAA	CCT	GTC	ATG	1994
Val	Val	Glu	Gly	Thr	Ala	Tyr	Gly	Leu	Ser	Arg	Ser	Gln	Pro	Val	Met	
			610					615					620			
AAA	GTT	GCA	GTG	AAG	ATG	CTA	AAA	CCC	ACG	GCC	AGA	TCC	AGT	GAA	AAA	2042
Lys	Val	Ala	Val	Lys	Met	Leu	Lys	Pro	Thr	Ala	Arg	Ser	Ser	Glu	Lys	
		625					630					635				
CAA	GCT	CTC	ATG	TCT	GAA	CTG	AAG	ATA	ATG	ACT	CAC	CTG	GGG	CCA	CAT	2090
Gln	Ala	Leu	Met	Ser	Glu	Leu	Lys	Ile	Met	Thr	His	Leu	Gly	Pro	His	
		640				645					650					
TTG	AAC	ATT	GTA	AAC	TTG	CTG	GGA	GCC	TGC	ACC	AAG	TCA	GGC	CCC	ATT	2138
Leu	Asn	Ile	Val	Asn	Leu	Leu	Gly	Ala	Cys	Thr	Lys	Ser	Gly	Pro	Ile	
655					660					665					670	
TAC	ATC	ATC	ACA	GAG	TAT	TGC	TTC	TAT	GGA	GAT	TTG	GTC	AAC	TAT	TTG	2186
Tyr	Ile	Ile	Thr	Glu	Tyr	Cys	Phe	Tyr	Gly	Asp	Leu	Val	Asn	Tyr	Leu	
				675					680					685		
CAT	AAG	AAT	AGG	GAT	AGC	TTC	CTG	AGC	CAC	CAC	CCA	GAG	AAG	CCA	AAG	2234
His	Lys	Asn	Arg	Asp	Ser	Phe	Leu	Ser	His	His	Pro	Glu	Lys	Pro	Lys	
			690					695					700			
AAA	GAG	CTG	GAT	ATC	TTT	GGA	TTG	AAC	CCT	GCT	GAT	GAA	AGC	ACA	CGG	2282
Lys	Glu	Leu	Asp	Ile	Phe	Gly	Leu	Asn	Pro	Ala	Asp	Glu	Ser	Thr	Arg	
		705					710					715				
AGC	TAT	GTT	ATT	TTA	TCT	TTT	GAA	AAC	AAT	GGT	GAC	TAC	ATG	GAC	ATG	2330
Ser	Tyr	Val	Ile	Leu	Ser	Phe	Glu	Asn	Asn	Gly	Asp	Tyr	Met	Asp	Met	
	720					725					730					
AAG	CAG	GCT	GAT	ACT	ACA	CAG	TAT	GTC	CCC	ATG	CTA	GAA	AGG	AAA	GAG	2378
Lys	Gln	Ala	Asp	Thr	Thr	Gln	Tyr	Val	Pro	Met	Leu	Glu	Arg	Lys	Glu	
735					740					745					750	
GTT	TCT	AAA	TAT	TCC	GAC	ATC	CAG	AGA	TCA	CTC	TAT	GAT	CGT	CCA	GCC	2426
Val	Ser	Lys	Tyr	Ser	Asp	Ile	Gln	Arg	Ser	Leu	Tyr	Asp	Arg	Pro	Ala	
				755					760					765		
TCA	TAT	AAG	AAG	AAA	TCT	ATG	TTA	GAC	TCA	GAA	GTC	AAA	AAC	CTC	CTT	2474
Ser	Tyr	Lys	Lys	Lys	Ser	Met	Leu	Asp	Ser	Glu	Val	Lys	Asn	Leu	Leu	
			770					775					780			
TCA	GAT	GAT	AAC	TCA	GAA	GGC	CTT	ACT	TTA	TTG	GAT	TTG	TTG	AGC	TTC	2522
Ser	Asp	Asp	Asn	Ser	Glu	Gly	Leu	Thr	Leu	Leu	Asp	Leu	Leu	Ser	Phe	
		785					790					795				

ACC	TAT	CAA	GTT	GCC	CGA	GGA	ATG	GAG	TTT	TTG	GCT	TCA	AAA	AAT	TGT	2570
Thr	Tyr	Gln	Val	Ala	Arg	Gly	Met	Glu	Phe	Leu	Ala	Ser	Lys	Asn	Cys	
800						805					810					
GTC	CAC	CGT	GAT	CTG	GCT	GCT	CGC	AAC	GTT	CTC	CTG	GCA	CAA	GGA	AAA	2618
Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Val	Leu	Leu	Ala	Gln	Gly	Lys	
815					820					825					830	
ATT	GTG	AAG	ATC	TGT	GAC	TTT	GGC	CTG	GCC	AGA	GAC	ATC	ATG	CAT	GAT	2666
Ile	Val	Lys	Ile	Cys	Asp	Phe	Gly	Leu	Ala	Arg	Asp	Ile	Met	His	Asp	
				835					840					845		
TCG	AAC	TAT	GTG	TCG	AAA	GGC	AGT	ACC	TTT	CTG	CCC	GTG	AAG	TGG	ATG	2714
Ser	Asn	Tyr	Val	Ser	Lys	Gly	Ser	Thr	Phe	Leu	Pro	Val	Lys	Trp	Met	
			850					855						860		
GCT	CCT	GAG	AGC	ATC	TTT	GAC	AAC	CTC	TAC	ACC	ACA	CTG	AGT	GAT	GTC	2762
Ala	Pro	Glu	Ser	Ile	Phe	Asp	Asn	Leu	Tyr	Thr	Thr	Leu	Ser	Asp	Val	
		865					870					875				
TGG	TCT	TAT	GGC	ATT	CTG	CTC	TGG	GAG	ATC	TTT	TCC	CTT	GGT	GGC	ACC	2810
Trp	Ser	Tyr	Gly	Ile	Leu	Leu	Trp	Glu	Ile	Phe	Ser	Leu	Gly	Gly	Thr	
	880					885					890					
CCT	TAC	CCC	GGC	ATG	ATG	GTG	GAT	TCT	ACT	TTC	TAC	AAT	AAG	ATC	AAG	2858
Pro	Tyr	Pro	Gly	Met	Met	Val	Asp	Ser	Thr	Phe	Tyr	Asn	Lys	Ile	Lys	
895					900					905					910	
AGT	GGG	TAC	CGG	ATG	GCC	AAG	CCT	GAC	CAC	GCT	ACC	AGT	GAA	GTC	TAC	2906
Ser	Gly	Tyr	Arg	Met	Ala	Lys	Pro	Asp	His	Ala	Thr	Ser	Glu	Val	Tyr	
				915					920					925		
GAG	ATC	ATG	GTG	AAA	TGC	TGG	AAC	AGT	GAG	CCG	GAG	AAG	AGA	CCC	TCC	2954
Glu	Ile	Met	Val	Lys	Cys	Trp	Asn	Ser	Glu	Pro	Glu	Lys	Arg	Pro	Ser	
			930					935					940			
TTT	TAC	CAC	CTG	AGT	GAG	ATT	GTG	GAG	AAT	CTG	CTG	CCT	GGA	CAA	TAT	3002
Phe	Tyr	His	Leu	Ser	Glu	Ile	Val	Glu	Asn	Leu	Leu	Pro	Gly	Gln	Tyr	
		945					950					955				
AAA	AAG	AGT	TAT	GAA	AAA	ATT	CAC	CTG	GAC	TTC	CTG	AAG	AGT	GAC	CAT	3050
Lys	Lys	Ser	Tyr	Glu	Lys	Ile	His	Leu	Asp	Phe	Leu	Lys	Ser	Asp	His	
	960					965					970					
CCT	GCT	GTG	GCA	CGC	ATG	CGT	GTG	GAC	TCA	GAC	AAT	GCA	TAC	ATT	GGT	3098
Pro	Ala	Val	Ala	Arg	Met	Arg	Val	Asp	Ser	Asp	Asn	Ala	Tyr	Ile	Gly	
975					980					985					990	
GTC	ACC	TAC	AAA	AAC	GAG	GAA	GAC	AAG	CTG	AAG	GAC	TGG	GAG	GGT	GGT	3146
Val	Thr	Tyr	Lys	Asn	Glu	Glu	Asp	Lys	Leu	Lys	Asp	Trp	Glu	Gly	Gly	
				995					1000					1005		
CTG	GAT	GAG	CAG	AGA	CTG	AGC	GCT	GAC	AGT	GGC	TAC	ATC	ATT	CCT	CTG	3194
Leu	Asp	Glu	Gln	Arg	Leu	Ser	Ala	Asp	Ser	Gly	Tyr	Ile	Ile	Pro	Leu	
			1010					1015					1020			
CCT	GAC	ATT	GAC	CCT	GTC	CCT	GAG	GAG	GAG	GAC	CTG	GGC	AAG	AGG	AAC	3242
Pro	Asp	Ile	Asp	Pro	Val	Pro	Glu	Glu	Glu	Asp	Leu	Gly	Lys	Arg	Asn	
		1025					1030					1035				
AGA	CAC	AGC	TCG	CAG	ACC	TCT	GAA	GAG	AGT	GCC	ATT	GAG	ACG	GGT	TCC	3290
Arg	His	Ser	Ser	Gln	Thr	Ser	Glu	Glu	Ser	Ala	Ile	Glu	Thr	Gly	Ser	
		1040				1045					1050					
AGC	AGT	TCC	ACC	TTC	ATC	AAG	AGA	GAG	GAC	GAG	ACC	ATT	GAA	GAC	ATC	3338
Ser	Ser	Ser	Thr	Phe	Ile	Lys	Arg	Glu	Asp	Glu	Thr	Ile	Glu	Asp	Ile	
1055					1060					1065					1070	

GAC ATG ATG GAC GAC ATC GGC ATA GAC TCT TCA GAC CTG GTG GAA GAC Asp Met Met Asp Asp Ile Gly Ile Asp Ser Ser Asp Leu Val Glu Asp 1075 1080 1085	3386
AGC TTC CTG TAA CTGGCGGATT CGAGGGGTTC CTTCCACTTC TGGGGCCACC Ser Phe Leu *	3438
1090	
TCTGGATCCC GTTCAGAAAA CCACTTTATT GCAATGCGGA GGTGAGAGG AGGACTTGGT	3498
TGATGTTTAA AGAGAAGTTC CCAGCCAAGG GCCTCGGGGA GCCTTTCTAA ATATGAATGA	3558
ATGGGATATT TTGAAATGAA CTTTGTCACT GTTGCCCTCTT GCAATGCCTC AGTAGCATCT	3618
CAGTGGTGTG TGAAGTTTGG AGATAGATGG ATAAGGGAAT AATAGGCCAC AGAAGGTGAA	3678
CTTCTGCTT CAAGGACATT GGTGAGAGTC CAACAGACAC AATTTATACT GCGACAGAAC	3738
TTCAGCATTG TAATTATGTA AATAACTCTA ACCACGGCTG TGTTTAGATT GTATTAACTA	3798
TCTTCTTTGG ACTTCTGAAG AGACCACTCA ATCCATCCAT GTACTTCCCT CTTGAAACCT	3858
GATGTCAGCT GCTGTTGAAC TTTTAAAGA AGTGCATGAA AAACCATTTT TGACCTTAAA	3918
AGGTACTGGT ACTATAGCAT TTTGCTATCT TTTTGTAGTGT TAAAGAGATA AAGAATAATA	3978
ATTAACCAAC CTTGTTTAAAT AGATTGGGT CATTTAGAAG CCTGACAACT CATTTTCATA	4038
TTGTAATCTA TGTTTATAAT ACTACTACTG TTATCAGTAA TGCTAAATGT GTAATAATGT	4098
AACATGATTT CCCTCCACAC AAAGCACAAAT TTAAAAACAA TCCTTACTAA GTAGGTGATG	4158
AGTTTGACAG TTTTGTGACAT TTATATTAAA TAACATGTTT CTCTATAAAG TATGGTAATA	4218
GCTTTAGTGA ATTAAATTTA GTTGAGCATA GAGAACAAAG TAAAGTAGT GTTGTCCAGG	4278
AAGTCAGAAT TTTTAACTGT ACTGAATAGG TTCCCAATC CATCGTATTA AAAACAATT	4338
AACTGCCCTC TGAAATAATG GGATTAGAAA CAAACAAAAC TCTTAAGTCC TAAAGTTCT	4398
CAATGTAGAG GCATAAACCT GTGCTGAACA TAACTTCTCA TGTATATTAC CCAATGGAAA	4458
ATATAATGAT CAGCGCAAAA GACTGGATTG GCAGAAGTTT TTTTTTTTTT TCTTCTTGCC	4518
TGATGAAAGC TTTGGCGACC CCAATATATG TATTTTTTGA ATCTATGAAC CTGAAAAGGG	4578
TCACAAAGGA TGCCCAGACA TCAGCCTCCT TCTTTCACCC CTTACCCCAA AGAGAAAGAG	4638
TTTGAACTC GAGACCATAA AGATATTCTT TAGTGGAGGC TGGAAAGTGA TTAGCCTGAT	4698
CCTCAGTTCT CAAATGTGTG TGGCAGCCAG GTAGACTAGT ACCTGGGTTT CCATCCTTGA	4758
GATTCTGAAG TATGAAGTCT GAGGGAAACC AGAGTCTGTA TTTTCTAAA CTCCCTGGCT	4818
GTTCTGATCG GCCAGGTTT GGAACACTG ACTTAGGTTT CAGGAAGTTG CCATGGGAAA	4878
CAAATAATTT GAACTTTGGA ACAGGGTTCT TAAGTTGGTG CGTCCTTCGG ATGATAAATT	4938
TAGGAACCGA AGTCCAATCA CTGTAAATTA CGGTAGATCG ATCGTTAACG CTGGAATTAA	4998
ATTGAAAGGT CAGAATCGAC TCCGACTCTT TCGATTTCAA ACCAAACTG TCCAAAAGGT	5058
TTTCATTTCT ACGATGAAGG GTGACATACC CCCTCTAACT TGAAAGGGGC AGAGGGCAGA	5118
AGAGCGGAGG GTGAGGTATG GGGCGGTTCC TTTCCGTACA TGTTTTTAAT ACGTTAAGTC	5178
ACAAGGTTCA GAGACACATT GGTCGAGTCA CAAAACCACC TTTTTTGTA AATTCAAAT	5238

GACTATTAAA CTCCAATCTA CCCTCCTACT TAACAGTGTA GATAGGTGTG ACAGTTTGTC 5298
 CAACCACACC CAAGTAACCG TAAGAAACGT TATGACGAAT TAACGACTAT GGTATACTTA 5358
 CTTTGTACCC GACACTAATG ACGTTAGTGA CACGATAGCC GTCTACTACG AAACCTTCTA 5418
 CGTCTTCGTT ATTATTTTCAT GAACTGATGG ATGACCACAT TAGAGTTACG TTCGGGGTTG 5478
 AAAGAATAGG TTGAAAAAGT ATCATTACAG CTTCTGACTC GGTCTAACCG GTTAATTTTT 5538
 CTTTTGGACT GATCCAAGAC ATCTCGGTGA ATCTGAACTT TATGCAAACA CAAAGATCTT 5598
 AGTGTCGAGT TCGTAAGACA AATAGCGAGT GAGAGGGAAC ATGTCGGAAT AAAACAACCA 5658
 CGAAACGTAA AACTATAACG ACACTCGGAA CGTACTGTAG TACTCCGGCC TACTTTGAAG 5718
 AGTCAGGTCG TCAAAGGTCA GGATTGTTTA CGAGGGTGGA CTTAAACATA TACTGACGTA 5778
 AACACCCACA CACACACAAA AGTCGTTTAA GGTCTAAACA AAGGAAAACC GGAGGACGTT 5838
 TCAGAGGTCT TCTTTTAAAC GGTTAGAAAG GATGAAAGAT AAAAATACTA CTGTTAGTTT 5898
 CGGCCGGACT CTTTGTGATA AACACTGAAA AATTGCTAA TCACTACAGG AATTTTACAC 5958
 CAGACGGTTA GACATGTTTT ACCAGGATAA AAACACTTCT CCCTGTATTC TATTTTACTA 6018
 CAATATGTAG TTATACATAT ATACATAAAG ATATATCTGA ACCTCTTATG ACGGTTTTGT 6078
 AAATACTGTT CGACATAGTG ACGGAAGCAA ATATAAAAAA ATTGACACTA TTAGGGGTGT 6138
 CCGTGTAATT GACAACGTGA AAACCTTACAG GTTTTAAATA TAAAATCTTT ATTATTTTTC 6198
 TTTCTATGAA TGTACAAGGG TTTTGTTACC ACACCACTTA CACACTCTTT TTGATTGAAC 6258
 TATCCCAGAT GGTATGTTT TACATAATGC TTACGGGGAC AAGTACAAA ACAAATTTT 6318
 GCACATTTAC TTCTAGAAAT ATAAAGTTAT TACTATATA TTAAATTTCC TTAAG 6373

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1090 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Thr Ser His Pro Ala Phe Leu Val Leu Gly Cys Leu Leu Thr
 1 5 10 15
 Gly Leu Ser Leu Ile Leu Cys Gln Leu Ser Leu Pro Ser Ile Leu Pro
 20 25 30
 Asn Glu Asn Glu Lys Val Val Gln Leu Asn Ser Ser Phe Ser Leu Arg
 35 40 45
 Cys Phe Gly Glu Ser Glu Val Ser Trp Gln Tyr Pro Met Ser Glu Glu
 50 55 60
 Glu Ser Ser Asp Val Glu Ile Arg Asn Glu Glu Asn Asn Ser Gly Leu
 65 70 75 80
 Phe Val Thr Val Leu Glu Val Ser Ser Ala Ser Ala Ala His Thr Gly
 85 90 95

Leu Tyr Thr Cys Tyr Tyr Asn His Thr Gln Thr Glu Glu Asn Glu Leu
 100 105 110
 Glu Gly Arg His Ile Tyr Ile Tyr Val Pro Asp Pro Asp Val Ala Phe
 115 120 125
 Val Pro Leu Gly Met Thr Asp Tyr Leu Val Ile Val Glu Asp Asp Asp
 130 135 140
 Ser Ala Ile Ile Pro Cys Arg Thr Thr Asp Pro Glu Thr Pro Val Thr
 145 150 155 160
 Leu His Asn Ser Glu Gly Val Val Pro Ala Ser Tyr Asp Ser Arg Gln
 165 170 175
 Gly Phe Asn Gly Thr Phe Thr Val Gly Pro Tyr Ile Cys Glu Ala Thr
 180 185 190
 Val Lys Gly Lys Lys Phe Gln Thr Ile Pro Phe Asn Val Tyr Ala Leu
 195 200 205
 Lys Ala Thr Ser Glu Leu Asp Leu Glu Met Glu Ala Leu Lys Thr Val
 210 215 220
 Tyr Lys Ser Gly Glu Thr Ile Val Val Thr Cys Ala Val Phe Asn Asn
 225 230 235 240
 Glu Val Val Asp Leu Gln Trp Thr Tyr Pro Gly Glu Val Lys Gly Lys
 245 250 255
 Gly Ile Thr Met Leu Glu Glu Ile Lys Val Pro Ser Ile Lys Leu Val
 260 265 270
 Tyr Thr Leu Thr Val Pro Glu Ala Thr Val Lys Asp Ser Gly Asp Tyr
 275 280 285
 Glu Cys Ala Ala Arg Gln Ala Thr Arg Glu Val Lys Glu Met Lys Lys
 290 295 300
 Val Thr Ile Ser Val His Glu Lys Gly Phe Ile Glu Ile Lys Pro Thr
 305 310 315 320
 Phe Ser Gln Leu Glu Ala Val Asn Leu His Glu Val Lys His Phe Val
 325 330 335
 Val Glu Val Arg Ala Tyr Pro Pro Pro Arg Ile Ser Trp Leu Lys Asn
 340 345 350
 Asn Leu Thr Leu Ile Glu Asn Leu Thr Glu Ile Thr Thr Asp Val Glu
 355 360 365
 Lys Ile Gln Glu Ile Arg Tyr Arg Ser Lys Leu Lys Leu Ile Arg Ala
 370 375 380
 Lys Glu Glu Asp Ser Gly His Tyr Thr Ile Val Ala Gln Asn Glu Asp
 385 390 395 400
 Ala Val Lys Ser Tyr Thr Phe Glu Leu Leu Thr Gln Val Pro Ser Ser
 405 410 415
 Ile Leu Asp Leu Val Asp Asp His His Gly Ser Thr Gly Gly Gln Thr
 420 425 430
 Val Arg Cys Thr Ala Glu Gly Thr Pro Leu Pro Asp Ile Glu Trp Met
 435 440 445

Ile Cys Lys Asp Ile Lys Lys Cys Asn Asn Glu Thr Ser Trp Thr Ile
 450 455 460
 Leu Ala Asn Asn Val Ser Asn Ile Ile Thr Glu Ile His Ser Arg Asp
 465 470 475 480
 Arg Ser Thr Val Glu Gly Arg Val Thr Phe Ala Lys Val Glu Glu Thr
 485 490 495
 Ile Ala Val Arg Cys Leu Ala Lys Asn Leu Leu Gly Ala Glu Asn Arg
 500 505 510
 Glu Leu Lys Leu Val Ala Pro Thr Leu Arg Ser Glu Leu Thr Val Ala
 515 520 525
 Ala Ala Val Leu Val Leu Leu Val Ile Val Ile Ile Ser Leu Ile Val
 530 535 540
 Leu Val Val Ile Trp Lys Gln Lys Pro Arg Tyr Glu Ile Arg Trp Arg
 545 550 555 560
 Val Ile Glu Ser Ile Ser Pro Asp Gly His Glu Tyr Ile Tyr Val Asp
 565 570 575
 Pro Met Gln Leu Pro Tyr Asp Ser Arg Trp Glu Phe Pro Arg Asp Gly
 580 585 590
 Leu Val Leu Gly Arg Val Leu Gly Ser Gly Ala Phe Gly Lys Val Val
 595 600 605
 Glu Gly Thr Ala Tyr Gly Leu Ser Arg Ser Gln Pro Val Met Lys Val
 610 615 620
 Ala Val Lys Met Leu Lys Pro Thr Ala Arg Ser Ser Glu Lys Gln Ala
 625 630 635 640
 Leu Met Ser Glu Leu Lys Ile Met Thr His Leu Gly Pro His Leu Asn
 645 650 655
 Ile Val Asn Leu Leu Gly Ala Cys Thr Lys Ser Gly Pro Ile Tyr Ile
 660 665 670
 Ile Thr Glu Tyr Cys Phe Tyr Gly Asp Leu Val Asn Tyr Leu His Lys
 675 680 685
 Asn Arg Asp Ser Phe Leu Ser His His Pro Glu Lys Pro Lys Lys Glu
 690 695 700
 Leu Asp Ile Phe Gly Leu Asn Pro Ala Asp Glu Ser Thr Arg Ser Tyr
 705 710 715 720
 Val Ile Leu Ser Phe Glu Asn Asn Gly Asp Tyr Met Asp Met Lys Gln
 725 730 735
 Ala Asp Thr Thr Gln Tyr Val Pro Met Leu Glu Arg Lys Glu Val Ser
 740 745 750
 Lys Tyr Ser Asp Ile Gln Arg Ser Leu Tyr Asp Arg Pro Ala Ser Tyr
 755 760 765
 Lys Lys Lys Ser Met Leu Asp Ser Glu Val Lys Asn Leu Leu Ser Asp
 770 775 780
 Asp Asn Ser Glu Gly Leu Thr Leu L u Asp Leu Leu Ser Phe Thr Tyr
 785 790 795 800

Gln Val Ala Arg Gly Met Glu Phe Leu Ala Ser Lys Asn Cys Val His
 805 810 815
 Arg Asp Leu Ala Ala Arg Asn Val Leu Leu Ala Gln Gly Lys Ile Val
 820 825 830
 Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Met His Asp Ser Asn
 835 840 845
 Tyr Val Ser Lys Gly Ser Thr Phe Leu Pro Val Lys Trp Met Ala Pro
 850 855 860
 Glu Ser Ile Phe Asp Asn Leu Tyr Thr Thr Leu Ser Asp Val Trp Ser
 865 870 875 880
 Tyr Gly Ile Leu Leu Trp Glu Ile Phe Ser Leu Gly Gly Thr Pro Tyr
 885 890 895
 Pro Gly Met Met Val Asp Ser Thr Phe Tyr Asn Lys Ile Lys Ser Gly
 900 905 910
 Tyr Arg Met Ala Lys Pro Asp His Ala Thr Ser Glu Val Tyr Glu Ile
 915 920 925
 Met Val Lys Cys Trp Asn Ser Glu Pro Glu Lys Arg Pro Ser Phe Tyr
 930 935 940
 His Leu Ser Glu Ile Val Glu Asn Leu Leu Pro Gly Gln Tyr Lys Lys
 945 950 955 960
 Ser Tyr Glu Lys Ile His Leu Asp Phe Leu Lys Ser Asp His Pro Ala
 965 970 975
 Val Ala Arg Met Arg Val Asp Ser Asp Asn Ala Tyr Ile Gly Val Thr
 980 985 990
 Tyr Lys Asn Glu Glu Asp Lys Leu Lys Asp Trp Glu Gly Gly Leu Asp
 995 1000 1005
 Glu Gln Arg Leu Ser Ala Asp Ser Gly Tyr Ile Ile Pro Leu Pro Asp
 1010 1015 1020
 Ile Asp Pro Val Pro Glu Glu Glu Asp Leu Gly Lys Arg Asn Arg His
 1025 1030 1035 1040
 Ser Ser Gln Thr Ser Glu Glu Ser Ala Ile Glu Thr Gly Ser Ser Ser
 1045 1050 1055
 Ser Thr Phe Ile Lys Arg Glu Asp Glu Thr Ile Glu Asp Ile Asp Met
 1060 1065 1070
 Met Asp Asp Ile Gly Ile Asp Ser Ser Asp Leu Val Glu Asp Ser Phe
 1075 1080 1085
 Leu *
 1090

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 187..3507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGTTCTCCTG AGCCTTCAGG AGCCTGCACC AGTCCTGCCT GTCCTTCTAC TCAGCTGTTA	60
CCCCTCTGG GACCAGCAGT CTTTCTGATA ACTGGGAGAG GGCAGTAAGG AGGACTTCCT	120
GGAGGGGGTG ACTGTCCAGA GCCTGGAAC TGTGCCACAC CAGAAGCCAT CAGCAGCAAG	180
GACACC ATG CGG CTT CCG GGT GCG ATG CCA GCT CTG GCC CTC AAA GGC	228
Met Arg Leu Pro Gly Ala Met Pro Ala Leu Ala Leu Lys Gly	
1095 1100	
GAG CTG CTG TTG CTG TCT CTC CTG TTA CTT CTG GAA CCA CAG ATC TCT	276
Glu Leu Leu Leu Leu Ser Leu Leu Leu Leu Leu Glu Pro Gln Ile Ser	
1105 1110 1115 1120	
CAG GGC CTG GTC GTC ACA CCC CCG GGG CCA GAG CTT GTC CTC AAT GTC	324
Gln Gly Leu Val Val Thr Pro Pro Gly Pro Glu Leu Val Leu Asn Val	
1125 1130 1135	
TCC AGC ACC TTC GTT CTG ACC TGC TCG GGT TCA GCT CCG GTG GTG TGG	372
Ser Ser Thr Phe Val Leu Thr Cys Ser Gly Ser Ala Pro Val Val Trp	
1140 1145 1150	
GAA CGG ATG TCC CAG GAG CCC CCA CAG GAA ATG GCC AAG GCC CAG GAT	420
Glu Arg Met Ser Gln Glu Pro Pro Gln Glu Met Ala Lys Ala Gln Asp	
1155 1160 1165	
GGC ACC TTC TCC AGC GTG CTC ACA CTG ACC AAC CTC ACT GGG CTA GAC	468
Gly Thr Phe Ser Ser Val Leu Thr Leu Thr Asn Leu Thr Gly Leu Asp	
1170 1175 1180	
ACG GGA GAA TAC TTT TGC ACC CAC AAT GAC TCC CGT GGA CTG GAG ACC	516
Thr Gly Glu Tyr Phe Cys Thr His Asn Asp Ser Arg Gly Leu Glu Thr	
1185 1190 1195 1200	
GAT GAG CGG AAA CGG CTC TAC ATC TTT GTG CCA GAT CCC ACC GTG GGC	564
Asp Glu Arg Lys Arg Leu Tyr Ile Phe Val Pro Asp Pro Thr Val Gly	
1205 1210 1215	
TTC CTC CCT AAT GAT GCC GAG GAA CTA TTC ATC TTT CTC ACG GAA ATA	612
Phe Leu Pro Asn Asp Ala Glu Glu Leu Phe Ile Phe Leu Thr Glu Ile	
1220 1225 1230	
ACT GAG ATC ACC ATT CCA TGC CGA GTA ACA GAC CCA CAG CTG GTG GTG	660
Thr Glu Ile Thr Ile Pro Cys Arg Val Thr Asp Pro Gln Leu Val Val	
1235 1240 1245	
ACA CTG CAC GAG AAG AAA GGG GAC GTT GCA CTG CCT GTC CCC TAT GAT	708
Thr Leu His Glu Lys Lys Gly Asp Val Ala Leu Pro Val Pro Tyr Asp	
1250 1255 1260	
CAC CAA CGT GGC TTT TCT GGT ATC TTT GAG GAC AGA AGC TAC ATC TGC	756
His Gln Arg Gly Phe Ser Gly Ile Phe Glu Asp Arg Ser Tyr Ile Cys	
1265 1270 1275 1280	
AAA ACC ACC ATT GGG GAC AGG GAG GTG GAT TCT GAT GCC TAC TAT GTC	804
Lys Thr Thr Ile Gly Asp Arg Glu Val Asp Ser Asp Ala Tyr Tyr Val	
1285 1290 1295	

TAC AGA CTC CAG GTG TCA TCC ATC AAC GTC TCT GTG AAC GCA GTG CAG Tyr Arg Leu Gln Val Ser Ser Ile Asn Val Ser Val Asn Ala Val Gln 1300 1305 1310	852
ACT GTG GTC CGC CAG GGT GAG AAC ATC ACC CTC ATG TGC ATT GTG ATC Thr Val Val Arg Gln Gly Glu Asn Ile Thr Leu Met Cys Ile Val Ile 1315 1320 1325	900
GGG AAT GAT GTG GTC AAC TTC GAG TGG ACA TAC CCC CGC AAA GAA AGT Gly Asn Asp Val Val Asn Phe Glu Trp Thr Tyr Pro Arg Lys Glu Ser 1330 1335 1340	948
GGG CGG CTG GTG GAG CCG GTG ACT GAC TTC CTC TTG GAT ATG CCT TAC Gly Arg Leu Val Glu Pro Val Thr Asp Phe Leu Leu Asp Met Pro Tyr 1345 1350 1355 1360	996
CAC ATC CGC TCC ATC CTG CAC ATC CCC AGT GCC GAG TTA GAA GAC TCG His Ile Arg Ser Ile Leu His Ile Pro Ser Ala Glu Leu Glu Asp Ser 1365 1370 1375	1044
GGG ACC TAC ACC TGC AAT GTG ACG GAG AGT GTG AAT GAC CAT CAG GAT Gly Thr Tyr Thr Cys Asn Val Thr Glu Ser Val Asn Asp His Gln Asp 1380 1385 1390	1092
GAA AAG GCC ATC AAC ATC ACC GTG GTT GAG AGC GGC TAC GTG CGG CTC Glu Lys Ala Ile Asn Ile Thr Val Val Glu Ser Gly Tyr Val Arg Leu 1395 1400 1405	1140
CTG GGA GAG GTG GGC ACA CTA CAA TTT GCT GAG CTG CAT CGG AGC CGG Leu Gly Glu Val Gly Thr Leu Gln Phe Ala Glu Leu His Arg Ser Arg 1410 1415 1420	1188
ACA CTG CAG GTA GTG TTC GAG GCC TAC CCA CCG CCC ACT GTC CTG TGG Thr Leu Gln Val Val Phe Glu Ala Tyr Pro Pro Pro Thr Val Leu Trp 1425 1430 1435 1440	1236
TTC AAA GAC AAC CGC ACC CTG GGC GAC TCC AGC GCT GGC GAA ATC GCC Phe Lys Asp Asn Arg Thr Leu Gly Asp Ser Ser Ala Gly Glu Ile Ala 1445 1450 1455	1284
CTG TCC ACG CGC AAC GTG TCG GAG ACC CGG TAT GTG TCA GAG CTG ACA Leu Ser Thr Arg Asn Val Ser Glu Thr Arg Tyr Val Ser Glu Leu Thr 1460 1465 1470	1332
CTG GTT CGC GTG AAG GTG GCA GAG GCT GGC CAC TAC ACC ATG CGG GCC Leu Val Arg Val Lys Val Ala Glu Ala Gly His Tyr Thr Met Arg Ala 1475 1480 1485	1380
TTC CAT GAG GAT GCT GAG GTC CAG CTC TCC TTC CAG CTA CAG ATC AAT Phe His Glu Asp Ala Glu Val Gln Leu Ser Phe Gln Leu Gln Ile Asn 1490 1495 1500	1428
GTC CCT GTC CGA GTG CTG GAG CTA AGT GAG AGC CAC CCT GAC AGT GGG Val Pro Val Arg Val Leu Glu Leu Ser Glu Ser His Pro Asp Ser Gly 1505 1510 1515 1520	1476
GAA CAG ACA GTC CGC TGT CGT GGC CGG GGC ATG CCG CAG CCG AAC ATC Glu Gln Thr Val Arg Cys Arg Gly Arg Gly Met Pro Gln Pro Asn Ile 1525 1530 1535	1524
ATC TGG TCT GCC TGC AGA GAC CTC AAA AGG TGT CCA CGT GAG CTG CCG Ile Trp Ser Ala Cys Arg Asp Leu Lys Arg Cys Pro Arg Glu Leu Pro 1540 1545 1550	1572
CCC ACG CTG CTG GGG AAC AGT TCC GAA GAG GAG AGC CAG CTG GAG ACT Pro Thr Leu Leu Gly Asn Ser Ser Glu Glu Glu Ser Gln Leu Glu Thr 1555 1560 1565	1620

TAT	GTG	CCC	ATG	CTG	GAC	ATG	AAA	GGA	GAC	GTC	AAA	TAT	GCA	GAC	ATC	2484
Tyr	Val	Pro	Met	Leu	Asp	Met	Lys	Gly	Asp	Val	Lys	Tyr	Ala	Asp	Ile	
				1845					1850					1855		
GAG	TCC	TCC	AAC	TAC	ATG	GCC	CCT	TAC	GAT	AAC	TAC	GTT	CCC	TCT	GCC	2532
Glu	Ser	Ser	Asn	Tyr	Met	Ala	Pro	Tyr	Asp	Asn	Tyr	Val	Pro	Ser	Ala	
			1860					1865					1870			
CCT	GAG	AGG	ACC	TGC	CGA	GCA	ACT	TTG	ATC	AAC	GAG	TCT	CCA	GTG	CTA	2580
Pro	Glu	Arg	Thr	Cys	Arg	Ala	Thr	Leu	Ile	Asn	Glu	Ser	Pro	Val	Leu	
		1875					1880					1885				
AGC	TAC	ATG	GAC	CTC	GTG	GGC	TTC	AGC	TAC	CAG	GTG	GCC	AAT	GGC	ATG	2628
Ser	Tyr	Met	Asp	Leu	Val	Gly	Phe	Ser	Tyr	Gln	Val	Ala	Asn	Gly	Met	
	1890					1895					1900					
GAG	TTT	CTG	GCC	TCC	AAG	AAC	TGC	GTC	CAC	AGA	GAC	CTG	GCG	GCT	AGG	2676
Glu	Phe	Leu	Ala	Ser	Lys	Asn	Cys	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	
1905					1910					1915					1920	
AAC	GTG	CTC	ATC	TGT	GAA	GGC	AAG	CTG	GTC	AAG	ATC	TGT	GAC	TTT	GGC	2724
Asn	Val	Leu	Ile	Cys	Glu	Gly	Lys	Leu	Val	Lys	Ile	Cys	Asp	Phe	Gly	
				1925					1930					1935		
CTG	GCT	CGA	GAC	ATC	ATG	CGG	GAC	TCG	AAT	TAC	ATC	TCC	AAA	GGC	AGC	2772
Leu	Ala	Arg	Asp	Ile	Met	Arg	Asp	Ser	Asn	Tyr	Ile	Ser	Lys	Gly	Ser	
			1940					1945					1950			
ACC	TTT	TTG	CCT	TTA	AAG	TGG	ATG	GCT	CCG	GAG	AGC	ATC	TTC	AAC	AGC	2820
Thr	Phe	Leu	Pro	Leu	Lys	Trp	Met	Ala	Pro	Glu	Ser	Ile	Phe	Asn	Ser	
		1955					1960					1965				
CTC	TAC	ACC	ACC	CTG	AGC	GAC	GTG	TGG	TCC	TTC	GGG	ATC	CTG	CTC	TGG	2868
Leu	Tyr	Thr	Thr	Leu	Ser	Asp	Val	Trp	Ser	Phe	Gly	Ile	Leu	Leu	Trp	
	1970					1975					1980					
GAG	ATC	TTC	ACC	TTG	GGT	GGC	ACC	CCT	TAC	CCA	GAG	CTG	CCC	ATG	AAC	2916
Glu	Ile	Phe	Thr	Leu	Gly	Gly	Thr	Pro	Tyr	Pro	Glu	Leu	Pro	Met	Asn	
1985					1990					1995				2000		
GAG	CAG	TTC	TAC	AAT	GCC	ATC	AAA	CGG	GGT	TAC	CGC	ATG	GCC	CAG	CCT	2964
Glu	Gln	Phe	Tyr	Asn	Ala	Ile	Lys	Arg	Gly	Tyr	Arg	Met	Ala	Gln	Pro	
				2005					2010				2015			
GCC	CAT	GCC	TCC	GAC	GAG	ATC	TAT	GAG	ATC	ATG	CAG	AAG	TGC	TGG	GAA	3012
Ala	His	Ala	Ser	Asp	Glu	Ile	Tyr	Glu	Ile	Met	Gln	Lys	Cys	Trp	Glu	
			2020					2025					2030			
GAG	AAG	TTT	GAG	ATT	CGG	CCC	CCC	TTC	TCC	CAG	CTG	GTG	CTG	CTT	CTC	3060
Glu	Lys	Phe	Glu	Ile	Arg	Pro	Pro	Phe	Ser	Gln	Leu	Val	Leu	Leu	Leu	
		2035					2040					2045				
GAG	AGA	CTG	TTG	GGC	GAA	GGT	TAC	AAA	AAG	AAG	TAC	CAG	CAG	GTG	GAT	3108
Glu	Arg	Leu	Leu	Gly	Glu	Gly	Tyr	Lys	Lys	Lys	Tyr	Gln	Gln	Val	Asp	
	2050					2055					2060					
GAG	GAG	TTT	CTG	AGG	AGT	GAC	CAC	CCA	GCC	ATC	CTT	CGG	TCC	CAG	GCC	3156
Glu	Glu	Phe	Leu	Arg	Ser	Asp	His	Pro	Ala	Ile	Leu	Arg	Ser	Gln	Ala	
2065					2070					2075				2080		
CGC	TTG	CCT	GGG	TTC	CAT	GGC	CTC	CGA	TCT	CCC	CTG	GAC	ACC	AGC	TCC	3204
Arg	Leu	Pro	Gly	Phe	His	Gly	Leu	Arg	Ser	Pro	Leu	Asp	Thr	Ser	Ser	
			2085					2090					2095			
GTC	CTC	TAT	ACT	GCC	GTG	CAG	CCC	AAT	GAG	GGT	GAC	AAC	GAC	TAT	ATC	3252
Val	Leu	Tyr	Thr	Ala	Val	Gln	Pro	Asn	Glu	Gly	Asp	Asn	Asp	Tyr	Ile	
			2100					2105					2110			

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GGTCTGCGTC GAAGACAGAA TGGACAGTGA GGACAGTTAT GTCTTGTAAG AGACAAGAAG      4927
CTTCAGATGG GTACCCCAAG AAGGATGTGA GAGGTGGGCG CTTTGGAGGT TTGCCCCCTCA      4987
CCCACCAGCT GCCCCATCCC TGAGGCAGCG CTCCATGGGG GTATGGTTTT GTCAGTCCCC      5047
AGACCTAGCA GTGACATCTC ATTGTCCCCA GCCCAGTGGG CATTGGAGGT GCCAGGGGAG      5107
TCAGGGTTGT AGCCAAGACG CCCCCGCACG GGGAGGGTTG GGAAGGGGGT GCAGGAAGCT      5167
CAACCCCTCT GGGCACCAAC CCTGCATTGC AGGTGGGCAC CTTACTTCCC TGGGATCCCA      5227
GAGTTGGTCC AAGGAGGGAG AGTGGGTCTT CAATACGGTA CCAAGATAT AATCACCTAG      5287
GTTTACAAAT ATTTTATAGGA CTCACGTAA CTCACATTA TACAGCAGAA ATGCTATTTT      5347
GTATGCTGTT AAGTTTTTCT ATCTGTGTAC TTTTTTTTAA GGGAAAGATT TTAATATTAA      5407
ACCTGGTGCT TCTCACTCAC                                          5427

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1107 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Met Arg Leu Pro Gly Ala Met Pro Ala Leu Ala Leu Lys Gly Glu Leu
 1              5              10              15
Leu Leu Leu Ser Leu Leu Leu Leu Leu Glu Pro Gln Ile Ser Gln Gly
      20              25              30
Leu Val Val Thr Pro Pro Gly Pro Glu Leu Val Leu Asn Val Ser Ser
      35              40              45
Thr Phe Val Leu Thr Cys Ser Gly Ser Ala Pro Val Val Trp Glu Arg
      50              55              60
Met Ser Gln Glu Pro Pro Gln Glu Met Ala Lys Ala Gln Asp Gly Thr
      65              70              75              80
Phe Ser Ser Val Leu Thr Leu Thr Asn Leu Thr Gly Leu Asp Thr Gly
      85              90              95
Glu Tyr Phe Cys Thr His Asn Asp Ser Arg Gly Leu Glu Thr Asp Glu
      100              105              110
Arg Lys Arg Leu Tyr Ile Phe Val Pro Asp Pro Thr Val Gly Phe Leu
      115              120              125
Pro Asn Asp Ala Glu Glu Leu Phe Ile Phe Leu Thr Glu Ile Thr Glu
      130              135              140
Ile Thr Ile Pro Cys Arg Val Thr Asp Pro Gln Leu Val Val Thr Leu
      145              150              155              160
His Glu Lys Lys Gly Asp Val Ala Leu Pro Val Pro Tyr Asp His Gln
      165              170              175
Arg Gly Phe Ser Gly Ile Phe Glu Asp Arg Ser Tyr Ile Cys Lys Thr
      180              185              190

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Thr Ile Gly Asp Arg Glu Val Asp Ser Asp Ala Tyr Tyr Val Tyr Arg
 195 200 205
 Leu Gln Val Ser Ser Ile Asn Val Ser Val Asn Ala Val Gln Thr Val
 210 215 220
 Val Arg Gln Gly Glu Asn Ile Thr Leu Met Cys Ile Val Ile Gly Asn
 225 230 235 240
 Asp Val Val Asn Phe Glu Trp Thr Tyr Pro Arg Lys Glu Ser Gly Arg
 245 250 255
 Leu Val Glu Pro Val Thr Asp Phe Leu Leu Asp Met Pro Tyr His Ile
 260 265 270
 Arg Ser Ile Leu His Ile Pro Ser Ala Glu Leu Glu Asp Ser Gly Thr
 275 280 285
 Tyr Thr Cys Asn Val Thr Glu Ser Val Asn Asp His Gln Asp Glu Lys
 290 295 300
 Ala Ile Asn Ile Thr Val Val Glu Ser Gly Tyr Val Arg Leu Leu Gly
 305 310 315 320
 Glu Val Gly Thr Leu Gln Phe Ala Glu Leu His Arg Ser Arg Thr Leu
 325 330 335
 Gln Val Val Phe Glu Ala Tyr Pro Pro Pro Thr Val Leu Trp Phe Lys
 340 345 350
 Asp Asn Arg Thr Leu Gly Asp Ser Ser Ala Gly Glu Ile Ala Leu Ser
 355 360 365
 Thr Arg Asn Val Ser Glu Thr Arg Tyr Val Ser Glu Leu Thr Leu Val
 370 375 380
 Arg Val Lys Val Ala Glu Ala Gly His Tyr Thr Met Arg Ala Phe His
 385 390 395 400
 Glu Asp Ala Glu Val Gln Leu Ser Phe Gln Leu Gln Ile Asn Val Pro
 405 410 415
 Val Arg Val Leu Glu Leu Ser Glu Ser His Pro Asp Ser Gly Glu Gln
 420 425 430
 Thr Val Arg Cys Arg Gly Arg Gly Met Pro Gln Pro Asn Ile Ile Trp
 435 440 445
 Ser Ala Cys Arg Asp Leu Lys Arg Cys Pro Arg Glu Leu Pro Pro Thr
 450 455 460
 Leu Leu Gly Asn Ser Ser Glu Glu Glu Ser Gln Leu Glu Thr Asn Val
 465 470 475 480
 Thr Tyr Trp Glu Glu Glu Gln Glu Phe Glu Val Val Ser Thr Leu Arg
 485 490 495
 Leu Gln His Val Asp Arg Pro Leu Ser Val Arg Cys Thr Leu Arg Asn
 500 505 510
 Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser Leu
 515 520 525
 Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu
 530 535 540

Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro
 545 550 555 560
 Arg Tyr Glu Il Arg Trp Lys Val Ile Glu Ser Val Ser Ser Asp Gly
 565 570 575
 His Glu Tyr Ile Tyr Val Asp Pro Met Gln Leu Pro Tyr Asp Ser Thr
 580 585 590
 Trp Glu Leu Pro Arg Asp Gln Leu Val Leu Gly Arg Thr Leu Gly Ser
 595 600 605
 Gly Ala Phe Gly Gln Val Val Glu Ala Thr Ala His Gly Leu Ser His
 610 615 620
 Ser Gln Ala Thr Met Lys Val Ala Val Lys Met Leu Lys Ser Thr Ala
 625 630 635 640
 Arg Ser Ser Glu Lys Gln Ala Leu Met Ser Glu Leu Lys Ile Met Ser
 645 650 655
 His Leu Gly Pro His Leu Asn Val Val Asn Leu Leu Gly Ala Cys Thr
 660 665 670
 Lys Gly Gly Pro Ile Tyr Ile Ile Thr Glu Tyr Cys Arg Tyr Gly Asp
 675 680 685
 Leu Val Asp Tyr Leu His Arg Asn Lys His Thr Phe Leu Gln His His
 690 695 700
 Ser Asp Lys Arg Arg Pro Ser Ala Glu Leu Tyr Ser Asn Ala Leu
 705 710 715 720
 Pro Val Gly Leu Pro Leu Pro Ser His Val Ser Leu Thr Gly Glu Ser
 725 730 735
 Asp Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Val Asp Tyr Val
 740 745 750
 Pro Met Leu Asp Met Lys Gly Asp Val Lys Tyr Ala Asp Ile Glu Ser
 755 760 765
 Ser Asn Tyr Met Ala Pro Tyr Asp Asn Tyr Val Pro Ser Ala Pro Glu
 770 775 780
 Arg Thr Cys Arg Ala Thr Leu Ile Asn Glu Ser Pro Val Leu Ser Tyr
 785 790 795 800
 Met Asp Leu Val Gly Phe Ser Tyr Gln Val Ala Asn Gly Met Glu Phe
 805 810 815
 Leu Ala Ser Lys Asn Cys Val His Arg Asp Leu Ala Ala Arg Asn Val
 820 825 830
 Leu Ile Cys Glu Gly Lys Leu Val Lys Ile Cys Asp Phe Gly Leu Ala
 835 840 845
 Arg Asp Ile Met Arg Asp Ser Asn Tyr Ile Ser Lys Gly Ser Thr Phe
 850 855 860
 Leu Pro Leu Lys Trp Met Ala Pro Glu Ser Ile Phe Asn Ser Leu Tyr
 865 870 875 880
 Thr Thr Leu Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile
 885 890 895

Phe Thr Leu Gly Gly Thr Pro Tyr Pro Glu Leu Pro Met Asn Glu Gln
 900 905 910
 Phe Tyr Asn Ala Ile Lys Arg Gly Tyr Arg Met Ala Gln Pro Ala His
 915 920 925
 Ala Ser Asp Glu Ile Tyr Glu Ile Met Gln Lys Cys Trp Glu Glu Lys
 930 935 940
 Phe Glu Ile Arg Pro Pro Phe Ser Gln Leu Val Leu Leu Leu Glu Arg
 945 950 955 960
 Leu Leu Gly Glu Gly Tyr Lys Lys Lys Tyr Gln Gln Val Asp Glu Glu
 965 970 975
 Phe Leu Arg Ser Asp His Pro Ala Ile Leu Arg Ser Gln Ala Arg Leu
 980 985 990
 Pro Gly Phe His Gly Leu Arg Ser Pro Leu Asp Thr Ser Ser Val Leu
 995 1000 1005
 Tyr Thr Ala Val Gln Pro Asn Glu Gly Asp Asn Asp Tyr Ile Ile Pro
 1010 1015 1020
 Leu Pro Asp Pro Lys Pro Glu Val Ala Asp Glu Gly Pro Leu Glu Gly
 1025 1030 1035 1040
 Ser Pro Ser Leu Ala Ser Ser Thr Leu Asn Glu Val Asn Thr Ser Ser
 1045 1050 1055
 Thr Ile Ser Cys Asp Ser Pro Leu Glu Pro Gln Asp Glu Pro Glu Pro
 1060 1065 1070
 Glu Pro Gln Leu Glu Leu Gln Val Glu Pro Glu Pro Glu Leu Glu Gln
 1075 1080 1085
 Leu Pro Asp Ser Gly Cys Pro Ala Pro Arg Ala Glu Ala Glu Asp Ser
 1090 1095 1100
 Phe Leu *
 1105

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Peptide Y719"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Ile Asp Tyr Val Pro
 1 5 10 15
 Met Leu Asp Met
 20

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Peptide Y719P. Contains a phosphate group at position 14."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Ile Asp Tyr Val Pro
 1 5 10 15

Met Leu Asp Met
 20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Peptide Y708P. Contains a phosphate group at position 3."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Ile Asp Tyr Val Pro
 1 5 10 15

Met Leu Asp Met
 20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "Peptide Y719P short."

Contains a phosphate group at position 11."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Asp Met Ser Lys Asp Glu Ser Ile Asp Tyr Val Pro Met Leu Asp
1 5 10 15

Met

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..13

(D) OTHER INFORMATION: /note= "Peptide Y708P short.
Contains a phosphate group at position 3."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Ile Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..20

(D) OTHER INFORMATION: /note= "Peptide Y708P/F719.
Contains a phosphate group at position 3."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Ile Asp Phe Val Pro
1 5 10 15

Met Leu Asp Met
20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

Asp Leu Gly Gly
20

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURES:

- (D) OTHER INFORMATION: /note= "N is A, C, G, or T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTTSCGNGCN GCCAGNTCSC GNTG